

AMENDMENTS TO THE DRAWINGS

Please replace the drawings with the attached formal drawing sheets (forty-six (46) different sheets, Figs. 1A-9E) submitted herewith.



Title: METHODS AND COMPOSITIONS
RELATING TO CD-39-LIKE POLYPEPTIDES
AND NUCLEIC ACIDS
Applicants: Chadwick et al.
Docket No. 28110/36120D
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ACGTTGACAC AGGAATGAAG AGTGATTGG CTGAATCTTC AAGCAGAGGC GATATTGACC 60
ATGTGCTTTT TAAATTGGCC TGCGTGACCC GCCCACTTGG TGTAAGAAGAA GAACCGGCCA 120
AAGGGAGGGC CTGAAGGACC TCCACAGGAG TGTGAGCAGC ACTGCTTCAG CAACAAAGCC 180
TCAGGTCCAC ATCTTGGGAA GAAT ATG GCC ACT TCC TGG GGG GCT GTC TTC 231
Met Ala Thr Ser Trp Gly Ala Val Phe
1 5
ATG CTG ATC ATA GCC TGC GTT GGC AGC ACT GTC TTC TAC AGA GAA CAG 279
Met Leu Ile Ile Ala Cys Val Gly Ser Thr Val Phe Tyr Arg Glu Gln
10 15 20 25
CAG ACC TGG TTT GAA GGT GTC TTC TTG TCT TCC ATG TGC CCC ATT AAT 327
Gln Thr Trp Phe Glu Gly Val Phe Leu Ser Ser Met Cys Pro Ile Asn
30 35 40
GTC AGT GCC GGC ACC TTT TAT GGA ATT ATG TTT GAT GCG GGC AGC ACT 375
Val Ser Ala Gly Thr Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr
45 50 55
GGA GCT CGG ATT CAT GTT TAC ACT TTT GTG CAG AAA ACA GCA GGA CAG 423
Gly Ala Arg Ile His Val Tyr Thr Phe Val Gln Lys Thr Ala Gly Gln
60 65 70

FIG. 1A



Title: METHODS AND COMPOSITIONS
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AND NUCLEIC ACIDS

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FIG. 1B

ctc ccc ttt ctg gaa ggt gaa att ttt gat tct gtg aag ccg gga ctt	471
Leu Pro Phe Leu Glu Gly Glu Ile Phe Asp Ser Val Lys Pro Gly Leu	
75 80 85	
TCT GCT TTT GTG GAT CAG CCC AAA CAG GGT GCT GAG ACT GTC CAG GAG	519
Ser Ala Phe Val Asp Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Glu	
90 95 100 105	
CTC TTG GAG GTG GCC AAA GAC TCG ATC CCC AGA AGC CAC TGG GAA AGG	567
Leu Leu Glu Val Ala Lys Asp Ser Ile Pro Arg Ser His Trp Glu Arg	
110 115 120	
ACC CCG GTG GTT CTG AAA GCA ACG GCC GGA CTC CGT TTG CTG CCT GAG	615
Thr Pro Val Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu	
125 130 135	
CAG AAA GCC CAG GCT CTG CTC TTG GAG GTA GAG GAG ATC TTC AAG AAT	663
Gln Lys Ala Gln Ala Leu Leu Leu Glu Val Glu Glu Ile Phe Lys Asn	
140 145 150	
TCA CCT TTC CTG GTC CCA GAT GGC AGC GTT AGC ATC ATG GAT GGG TCC	711
Ser Pro Phe Leu Val Pro Asp Gly Ser Val Ser Ile Met Asp Gly Ser	
155 160 165	



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FIG. 1C

TAT GAA GGC ATA CTA GCC TGG GTT ACC GTG AAC TTT CTA ACA GGT CAG	759
Tyr Glu Gly Ile Leu Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln	185
170 175 180	
CTG CAT GGT CGT GGC CAG GAG ACT GTG GGG ACC CTT GAC CTG GGG GGT	807
Leu His Gly Arg Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly	200
190 195	
GCC TCC ACC CAA ATC ACG TTT CTA CCC CAG TTT GAG AAA ACC CTG GAA	855
Ala Ser Thr Gln Ile Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu	215
205 210	
CAA ACA CCT AGG GGC TAC CTC ACT TCC TTT GAG ATG TTT AAC AGC ACT	903
Gln Thr Pro Arg Gly Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr	230
220 225	
TTT AAG CTC TAT ACA CAT AGT TAC TTG GGA TTT GGA CTG AAA GCT GCA	951
Phe Lys Leu Tyr Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala	245
235 240	
AGA CTG GCA ACT CTG GGA GCC CTG GAA GCA AAA GGG ACT GAT GGA CAT	999
Arg Leu Ala Thr Leu Gly Ala Leu Glu Ala Lys Gly Thr Asp Gly His	265
250 255 260	



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FIG. 1D

ACG TTT CGA AGT GCC TGT TTA CCA AGA TGG TTG GAA GCA GAG TGG ATC	1047
Thr Phe Arg Ser Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile	270 275 280
TTT GGG GGT GTG AAA TAC CAG TAT GGT AAC CAA GAA GGG GAG ATG	1095
Phe Gly Gly Val Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Met	285 290 295
GGC TTT GAA CCC TGC TAT GCG GAA GTG CTG AGG GTA GTA CAG GGG AAA	1143
Gly Phe Glu Pro Cys Tyr Ala Glu Val Leu Arg Val Val Gln Gly Lys	300 305 310
CTT CAC CAG CCA GAA GAA GTC CGA GGA AGC GCC TTC TAC GCT TTC TCT	1191
Leu His Gln Pro Glu Glu Val Arg Gly Ser Ala Phe Tyr Ala Phe Ser	315 320 325
TAC TAC TAC GAT GAT CGA GCC GCT GAC ACA CAC TTG ATC GAT TAT GAA AAG	1239
Tyr Tyr Tyr Asp Arg Ala Ala Asp Thr His Leu Ile Asp Tyr Glu Lys	330 335 340 345
GGC GGG GTT TTA AAA GTT GAA GAT TTT GAA AGA AAA GCC AGA GAA GTG	1287
Gly Gly Val Leu Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val	350 355 360



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TGT GAC AAC TTG GGG AGC TTC TCC TCG GGC AGT CCT TTC CTC TGC ATG	1335
Cys Asp Asn Leu Gly Ser Phe Ser Gly Ser Pro Phe Leu Cys Met	375
	365
GAC CTC ACT TAC ATC ACA GCC CTG TTG AAA GAT GGT TTG GGC TTT GCC	1383
Asp Leu Thr Tyr Ile Thr Ala Leu Leu Lys Asp Gly Leu Gly Phe Ala	390
	385
GAA CGG CAC CCT CTT ACA GCT CAC AAA GAA AGT GAA CAA CAT AGA GAC	1431
Glu Arg His Pro Leu Thr Ala His Lys Glu Ser Glu Gln His Arg Asp	405
	400
TGG TTG GGC CTT GGG GGC CAC CTT TCA CCT GCT CCA GTC TCT GGG CAT	1479
Trp Leu Gly Leu Gly His Leu Ser Pro Ala Pro Val Ser Gly His	425
	415
CAC CAG CTG AGG CCA AGC TCC ACC TCT GAA GCC TGC ATT TCT GAA CCA	1527
His Gln Leu Arg Pro Ser Ser Thr Ser Glu Ala Cys Ile Ser Glu Pro	440
	435
GTT TTC TCA CAG GAA GGC GTG GAC TCA GAG ACA TTT TCT GAC CTC TCT	1575
Val Phe Ser Gln Glu Gly Val Asp Ser Glu Thr Phe Ser Asp Leu Ser	455
	445
	450

FIG. 1E



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FIG. 1F

GGA AAA GCC TGG CCC GAA ACC CGT TAACTGGTTT TATAAGGAGG GAGGGGTTTT 1629
Gly Lys Ala Trp Pro Glu Thr Arg 465
460

TAGATGAGTC TTGCTCTTGA GCCTAGTGAT TTGGGCTTCA ATGATTGCA CATCTAATGT 1689

GAATAGCTCC TAACCACTTG GTGGGTGCAT GGCTGGCACC AGACTGTAAA TCTTTTGGGA 1749

TTCTTTGTAC AGAGTCCTGC AAAGGAAAAA AGAGAAAAGG TTTGGAACTC CATGCTAGAT 1809

TGCGAGTTCA GAGACAGGTC CCTGGGGACC AAAGAACAAAT CTCGTTTCAA CCCTTGGATG 1869

CCTCATTTGCT TTGAATGGAT TCATTTTTCG TTATAAGCTG ATTTACTGAA ATCCCATAAAC 1929

CCATCAATGC TGTAAATTTT TTTCTTCTTA CCCTTATTAC ATTCCCTACC CTAAAAGCCT 1989

GGGGAAATA CCTGGTTTTC CTTCCCATCT ATAATTGAGA AAGAGGGGGG AAAAGATACT 2049

GTATTAGAAT TTGTGTGATC CTGTGGCACA ATAGATCAAC CAACCCATTT AAAGCTTAAA 2109

AAAAAAAAAA

2119



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peaNTase 1	---MELLIKLITFLFSMPAITS SSQYLGNLLTSRKIFLKQEEISSYAVVFDAGSTGSR
potapyrase 1	MLNQNSHFIFIIIAIFLVLP LSLSKNVNAQIPLRRHLLSHESE --HYAVIFDAGSTGSR
mNTase 1	MATSWGAVFMIIACVGS TVFYREQQTWFEGVFLSSMCPINVSAGTFYGYIMFDAGSTGTR
YGDPase 1	KTPEDISILPVNDEPGYLQDSKTEQNYPELADAVK QTSQTCSEEHKYVIMIDAGSTGSR
peaNTase 57	IHVYHFNQNLDLLHIGKGV EYYNKIITPGLSSYANNPEQAAKSLIPLLEQAEDVVPDDLQP
potapyrase 59	VHVFRFDEKLGLLPIGN NIYFYMAT EPGLSSYAEDPKAAANSLEPLLDGAEGVVPQELQS
mNTase 61	IHVYTFVQKTAGQLP PFEGEIFDSVKPGLSAFVDQPKQGAETVQELLEVAKDSIPRSHWE
YGDPase 61	VHIYKFDVCTS --PPTLLDEKFDHLEPGLSSFD TDVGAANS LDPLLKVAMNYVPIKARS
peaNTase 117	KTPVRLGATAGLRLLNGDASEKILQSV RDMLSNRSTF -NVQPD AVSIIDGTOEGSYLWVT
potapyrase 119	ETPLELGATAGLRMLKGDAAEKILQAV RNLVKNOSTF -HSKDQWVTILDGTOEGSYMMAA
mNTase 121	RTPVV LKATAGLRLLPEQKAQALL LEVEEIFKN -SPF -LVPDG SVSIMDGSYEGILAWVT
YGDPase 119	CTPVA VXATAGLRLLGDAKSSKILSAVRD HLKDYPPFPV VEGDGVSIMGGDEEGVFAWIT

FIG. 2A



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peaNTase	176	<u>V</u> <u>N</u> <u>Y</u> <u>A</u> <u>L</u> <u>G</u> <u>N</u> <u>L</u> <u>G</u> <u>K</u> <u>K</u> <u>Y</u> <u>T</u> <u>K</u> - - <u>T</u> <u>V</u> <u>G</u> <u>V</u> <u>I</u> <u>D</u> <u>L</u> <u>G</u> <u>G</u> <u>S</u> <u>V</u> <u>Q</u> <u>M</u> <u>A</u> <u>Y</u> <u>A</u> <u>V</u> <u>S</u> <u>K</u> <u>K</u> <u>T</u> <u>A</u> <u>K</u> <u>N</u> <u>A</u> <u>P</u> <u>K</u> <u>V</u> <u>A</u> <u>D</u> <u>G</u> <u>D</u> <u>D</u> <u>P</u> <u>Y</u> <u>I</u> <u>K</u> <u>V</u> <u>V</u> <u>L</u> <u>K</u> <u>G</u>
potapyrase	178	<u>I</u> <u>N</u> <u>X</u> <u>L</u> <u>L</u> <u>G</u> <u>N</u> <u>L</u> <u>G</u> <u>K</u> <u>D</u> <u>Y</u> <u>K</u> <u>S</u> - - <u>T</u> <u>T</u> <u>A</u> <u>T</u> <u>I</u> <u>D</u> <u>L</u> <u>G</u> <u>G</u> <u>S</u> <u>V</u> <u>Q</u> <u>M</u> <u>A</u> <u>Y</u> <u>A</u> <u>I</u> <u>S</u> <u>N</u> <u>E</u> <u>Q</u> <u>F</u> <u>A</u> <u>K</u> <u>A</u> <u>P</u> <u>Q</u> <u>N</u> <u>E</u> <u>D</u> <u>G</u> - <u>E</u> <u>P</u> <u>Y</u> <u>V</u> <u>V</u> <u>Q</u> <u>K</u> <u>H</u> <u>L</u> <u>M</u> <u>S</u>
mNTase	179	<u>V</u> <u>N</u> <u>F</u> <u>L</u> <u>T</u> <u>G</u> <u>Q</u> <u>L</u> <u>H</u> <u>G</u> <u>R</u> <u>G</u> <u>Q</u> <u>E</u> - - <u>T</u> <u>V</u> <u>G</u> <u>T</u> <u>L</u> <u>D</u> <u>L</u> <u>G</u> <u>G</u> <u>A</u> <u>S</u> <u>T</u> <u>Q</u> <u>I</u> <u>T</u> <u>F</u> <u>L</u> <u>P</u> <u>O</u> <u>F</u> <u>E</u> <u>K</u> - - - - <u>T</u> <u>L</u> <u>E</u> <u>Q</u> <u>T</u> <u>P</u> <u>R</u> <u>G</u> <u>Y</u> <u>L</u> <u>T</u> <u>S</u> <u>F</u> <u>E</u> <u>M</u> <u>F</u> <u>N</u>
YGDase	179	<u>T</u> <u>N</u> <u>Y</u> <u>L</u> <u>L</u> <u>G</u> <u>N</u> <u>I</u> <u>G</u> <u>A</u> <u>N</u> <u>G</u> <u>P</u> <u>K</u> <u>L</u> <u>P</u> <u>T</u> <u>A</u> <u>A</u> <u>V</u> <u>F</u> <u>D</u> <u>L</u> <u>G</u> <u>G</u> <u>S</u> <u>T</u> <u>Q</u> <u>I</u> <u>V</u> <u>F</u> <u>E</u> <u>P</u> - - <u>T</u> <u>F</u> <u>P</u> <u>I</u> <u>N</u> <u>E</u> <u>K</u> <u>M</u> <u>V</u> <u>D</u> <u>G</u> <u>E</u> <u>H</u> <u>K</u> <u>F</u> - - <u>D</u> <u>L</u> <u>K</u> <u>F</u> <u>G</u> <u>D</u>
peaNTase	234	<u>I</u> <u>P</u> <u>Y</u> <u>D</u> <u>L</u> <u>Y</u> <u>V</u> <u>H</u> <u>S</u> <u>Y</u> <u>L</u> <u>H</u> <u>F</u> <u>G</u> <u>R</u> <u>E</u> <u>A</u> <u>S</u> <u>R</u> <u>A</u> <u>E</u> <u>I</u> <u>L</u> <u>K</u> <u>L</u> - - - - - <u>T</u> <u>P</u> <u>R</u> <u>S</u> <u>P</u> <u>N</u> <u>P</u> <u>C</u> <u>L</u> <u>L</u> <u>A</u> <u>G</u> <u>F</u> <u>N</u> <u>G</u> <u>I</u> <u>Y</u>
potapyrase	235	<u>K</u> <u>E</u> <u>Y</u> <u>N</u> <u>L</u> <u>Y</u> <u>V</u> <u>H</u> <u>S</u> <u>Y</u> <u>L</u> <u>N</u> <u>Y</u> <u>G</u> <u>Q</u> <u>L</u> <u>A</u> <u>G</u> <u>R</u> <u>A</u> <u>E</u> <u>I</u> <u>F</u> <u>K</u> <u>A</u> - - - - - <u>S</u> <u>R</u> <u>N</u> <u>E</u> <u>S</u> <u>N</u> <u>P</u> <u>C</u> <u>A</u> <u>L</u> <u>E</u> <u>G</u> <u>G</u> <u>D</u> <u>G</u> <u>Y</u> <u>Y</u>
mNTase	232	<u>S</u> <u>T</u> <u>F</u> <u>K</u> <u>L</u> <u>Y</u> <u>T</u> <u>H</u> <u>S</u> <u>Y</u> <u>L</u> <u>G</u> <u>F</u> <u>G</u> <u>L</u> <u>K</u> <u>A</u> <u>R</u> <u>L</u> <u>A</u> <u>T</u> <u>L</u> <u>G</u> <u>A</u> - - - - - <u>L</u> <u>E</u> <u>A</u> <u>K</u> <u>G</u> <u>T</u> - - - - <u>D</u> <u>G</u> <u>H</u> <u>T</u> <u>F</u> <u>R</u> <u>S</u>
YGDase	234	<u>E</u> <u>N</u> <u>Y</u> <u>T</u> <u>L</u> <u>Y</u> <u>Q</u> <u>F</u> <u>S</u> <u>H</u> <u>L</u> <u>G</u> <u>Y</u> <u>G</u> <u>L</u> <u>K</u> <u>E</u> <u>G</u> <u>R</u> <u>N</u> <u>K</u> <u>V</u> <u>N</u> <u>S</u> <u>V</u> <u>L</u> <u>V</u> <u>E</u> <u>N</u> <u>A</u> <u>L</u> <u>K</u> <u>D</u> <u>G</u> <u>K</u> <u>I</u> <u>L</u> <u>K</u> <u>G</u> <u>D</u> <u>N</u> <u>T</u> <u>K</u> <u>T</u> <u>H</u> <u>Q</u> <u>L</u> <u>S</u> <u>S</u> <u>P</u> <u>C</u> <u>L</u> <u>P</u> <u>P</u> <u>K</u> <u>V</u> <u>N</u> <u>A</u> <u>T</u> <u>N</u>
peaNTase	276	<u>T</u> <u>Y</u> <u>S</u> <u>G</u> <u>E</u> <u>E</u> <u>F</u> <u>K</u> <u>A</u> <u>T</u> <u>A</u> <u>Y</u> <u>T</u> <u>S</u> <u>G</u> <u>A</u> - - - - - <u>N</u> <u>F</u> <u>N</u> <u>K</u> <u>C</u> <u>K</u> <u>N</u> <u>T</u> <u>I</u> <u>R</u> <u>K</u> <u>A</u> <u>L</u> <u>K</u> <u>L</u> <u>N</u> <u>Y</u> <u>P</u> <u>C</u> <u>P</u> <u>Y</u> <u>Q</u> <u>N</u> <u>C</u> <u>T</u> <u>F</u> <u>G</u> <u>G</u> <u>I</u> <u>N</u> <u>G</u> <u>G</u> <u>G</u> <u>N</u> - - -
potapyrase	277	<u>S</u> <u>Y</u> <u>G</u> <u>G</u> <u>V</u> <u>D</u> <u>Y</u> <u>K</u> <u>V</u> <u>K</u> <u>A</u> <u>P</u> <u>K</u> <u>G</u> <u>S</u> - - - - - <u>S</u> <u>W</u> <u>K</u> <u>R</u> <u>C</u> <u>R</u> <u>R</u> <u>L</u> <u>T</u> <u>R</u> <u>H</u> <u>A</u> <u>L</u> <u>K</u> <u>I</u> <u>N</u> <u>A</u> <u>K</u> <u>C</u> <u>H</u> <u>I</u> <u>E</u> <u>E</u> <u>C</u> <u>T</u> <u>F</u> <u>N</u> <u>G</u> <u>V</u> <u>W</u> <u>N</u> <u>G</u> <u>G</u> <u>G</u> <u>D</u> - - -
mNTase	270	<u>A</u> <u>C</u> <u>L</u> <u>P</u> <u>R</u> <u>W</u> <u>L</u> <u>E</u> <u>A</u> <u>E</u> <u>W</u> <u>I</u> <u>F</u> <u>G</u> <u>C</u> <u>V</u> - - - - - <u>K</u> <u>Y</u> <u>Q</u> <u>Y</u> <u>G</u> <u>G</u> <u>N</u> <u>Q</u> <u>E</u> <u>G</u> <u>E</u> <u>M</u> <u>G</u> <u>F</u> <u>E</u> <u>P</u> <u>C</u> <u>Y</u> <u>A</u> <u>E</u> <u>V</u> <u>L</u> <u>R</u> <u>V</u> <u>V</u> <u>Q</u> <u>G</u> <u>K</u> <u>L</u> <u>H</u> <u>Q</u> <u>P</u> <u>E</u> <u>E</u> <u>V</u> <u>R</u> - - -
YGDase	294	<u>E</u> <u>K</u> <u>V</u> <u>T</u> <u>L</u> <u>E</u> <u>S</u> <u>K</u> <u>E</u> <u>T</u> <u>Y</u> <u>T</u> <u>I</u> <u>D</u> <u>F</u> <u>I</u> <u>G</u> <u>P</u> <u>D</u> <u>E</u> <u>P</u> <u>S</u> <u>G</u> <u>A</u> <u>Q</u> <u>C</u> <u>R</u> <u>F</u> <u>L</u> <u>T</u> <u>D</u> <u>E</u> <u>I</u> <u>L</u> <u>N</u> <u>K</u> <u>D</u> <u>A</u> <u>Q</u> <u>C</u> <u>Q</u> <u>S</u> <u>P</u> <u>P</u> <u>C</u> <u>S</u> <u>F</u> <u>N</u> <u>G</u> <u>V</u> <u>H</u> <u>Q</u> <u>P</u> <u>S</u> <u>L</u> <u>V</u> <u>R</u> <u>T</u> <u>F</u> <u>K</u>

FIG. 2B



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peaNTpase 328 GQKNLFASSFFYLPEDTGMVDASTPNFILRPVDIETKAKEACALNFEDAKSTYFFLDKK
potapyrase 329 GQKNIHASSFFYDIGAQVGIVDTKFPSALAKPIQYLNAAKVACQTNVADIKSIFPKTQDR
mNTpase 322 GSA-FYAFSYYYDRAADTHLIDYE-KGGVLKVEDFERKAREVCD-NLGSFSSGSP
YGDpase 354 ESNDIYIFSYFYDRTRPLGMPLSFTLNELDLARIVCKGEETWNSVPSGIAGS
peaNTpase 388 NVASYVCMDLIYQYVLLVDGFGLDPLQKITSGKEIEYQDAIVEAAWPLGNAVEAISALPK
potapyrase 389 NI-PYLCMDLIYEYTLLVDGFGLNPHKEITVIHDVQYKNYLVGAAWPLGCAIDLVSTTN
mNTpase 374 FLCMDLTYITALLKDGLGFAERHPLTANKEQHRDWLGLGHLSPAPVSGHHQLR
YGDpase 411 ESDSHFCLDLSFQVSLHTGYDIPLQRELRTGKKIANKE
peaNTpase 448 VERLMYFV
potapyrase 448 KIRVASS
mNTpase 430 PSSTSEACISEPVFSQEGVDSETFSDLSGKAWPETR
YGDpase 467 KCKIQSA

FIG. 2C



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FILE 3A



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ACR II

CD39	47	KY-VQKVNEIGI-YLTDCMERAREV	IPR---S-QHQETPVYLGATAGMRLLRMES	EEELAD
ratCD39	47	KY-AQKTDEIAA-YLAECMKMSTER	IPAAA-SKQHQ-TPVYLGATAGMRLLRMES	KQSAD
CD39L1	47	SY-ADNPSGASQ-SLVGCLQALQDVP	K---ER-HAGTPLYLGATAGMRLLNL	TNPEAST
chiATPase	47	SY-SSKPPAAGK-SLEHCLSQAMRDVP	K---EK-HADTPLYLGATAGMRLLT	IADPPSQT
peanTPase	46	SY-ANNPEQAAKS-LIPLLEQAEDVVP	---DDLQPKTPVRLGATAGLRLLN	--GDA-SE
potRRORP1	46	SY-AEDPKAAANS-LEPLLDGAEVVP	---QELQSETPLELGATAGLRMLK	--GDA-AE
YGDAL	44	SFDTDSV-GAANS-LDPILLKVAMNYVP	I---KARSCTPVAVKATAGLRLL	--GDAKSS
mNTase	46	AF-VDPQPKQGAET-VQELLEVAKDS	IPRSHWE--R--TPVVLLKATAGLRLL	---PEQKAQ
hCD39L2	10	AY-ADDVEKSAQG-IRELLDVAKQDIP	---FDSGRP-TPLVLLKATAGLRLL	---PGEKAQ
celegans	51	SFG-DKPEQVVE-YLTPLRRFAEENI	PYEQLGE---TDLLIFATAGMRLL	---PEAQKD
Y71KD	61	SFE-KKPQDAVKSHIKPILLDFAKNI	IPESHWS---CPVFIQATAGMRLL	---PQDIQS

FIG. 3B



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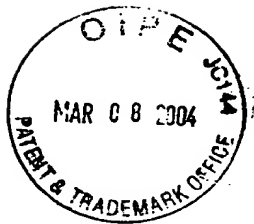
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		ACR III																																																					
CD39	101	RVL	D	V	V	E	R	S	L	S	N	-	YPP	---	DFQ	G	A	R	I	I	T	G	Q	E	E	G	A	Y	G	W	I	T	I	N	Y	L	L	G	K	F	S	Q	K	T	R	W	F	S	I	V	P				
ratCD39	101	EVL	A	A	V	S	R	S	L	K	S	-	YPP	---	DFQ	G	A	K	I	I	T	G	Q	E	E	G	A	Y	G	W	I	T	I	N	Y	L	L	G	R	F	T	Q	E	Q	S	W	L	N	F	I	S				
CD39L1	101	SVL	M	A	V	T	H	T	L	T	Q	-	YPP	---	DFR	G	A	R	I	L	S	G	Q	E	E	G	V	F	G	W	V	T	A	N	Y	L	L	E	N	F	I	-	K	Y	G	W	V	G	-	R					
chiATPase	101	-CL	S	A	V	M	A	T	L	K	S	-	YPP	---	DFG	G	A	K	I	L	S	G	E	E	G	V	F	G	W	I	T	A	N	Y	L	L	E	N	F	I	-	K	R	G	W	L	G	-	E						
peaNTase	97	KIL	Q	S	V	R	D	M	L	S	N	R	S	T	F	N	-	VQ	P	D	-	A	-	V	S	I	I	D	G	T	Q	E	G	S	Y	L	W	V	T	V	N	Y	A	L	G	N	---	L	---	G					
potRRP1	97	KIL	Q	A	V	R	N	L	V	K	N	Q	S	T	F	H	---	S	K	D	-	Q	W	V	T	I	L	D	G	T	Q	E	G	S	Y	M	W	A	A	I	N	Y	L	L	G	N	---	L	---	G					
yGDA1	95	KIL	S	A	V	R	D	H	L	E	K	D	Y	P	P	V	V	E	G	D	-	G	-	V	S	I	M	G	D	E	E	G	V	F	A	W	I	T	T	N	Y	L	L	G	N	---	I	G	A	N	G				
mNTase	97	ALL	L	E	V	E	E	I	F	-	K	N	S	P	F	-	L	V	-	P	D	-	G	S	V	S	I	M	D	G	S	E	G	I	L	A	W	V	T	V	N	F	L	T	G	---	L	H	G	R	G				
hCD39L2	61	KL	L	Q	K	V	K	E	Y	L	-	K	H	S	P	F	-	L	V	-	G	D	-	D	C	V	S	I	M	N	G	T	D	E	G	V	S	A	W	X	T	I	N	F	L	T	G	S	---	L	K	T	P	G	
celegans	102	A	I	K	N	L	Q	N	G	L	K	S	V	T	A	L	R	V	S	D	---	S	N	I	R	I	D	G	A	W	E	G	I	Y	S	W	I	A	V	N	Y	I	L	G	R	---	F	-	D	---					
y71KD	113	S	I	L	D	G	L	C	Q	G	L	K	H	P	A	E	F	L	V	E	D	C	S	-	A	Q	I	Q	V	I	D	G	E	T	E	G	L	Y	G	W	L	G	I	N	Y	L	Y	G	H	---	F	N	D	Y	N

FIG. 3C



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		ACR IV	
CD39	155	<u>YETNNQETFGALD</u>	<u>LGASTQVTFVPQNQ</u>
ratCD39	155	<u>-DSQKQATFGALD</u>	<u>LGGSSTQVTFVPLNQ</u>
CD39L1	152	<u>WFRPRKGTLGAMD</u>	<u>LGASTQITFETTSP</u>
chiATPase	151	<u>WIQSKKKT LGAMD</u>	<u>FGASTQITFETSDAI</u>
peantPase	144	<u>KKYTK--TVGVI</u>	<u>D LGGSVQ MAYAVSKK</u>
potRROP1	144	<u>KDYKS--TTATI</u>	<u>D LGGSVQ MAYAISNE</u>
YGDAl	146	<u>PKL-P--TAAVP</u>	<u>D LGGSSTQIVFEPTFPPI</u>
mNTPase	146	<u>QE-----TVGTL</u>	<u>D LGASTQITFLPQFE</u>
hCD39L2	110	<u>GS-----SVGML</u>	<u>D LGGSSTQIAFLPRVE</u>
celegans	149	<u>KE-NDS-KVGM</u>	<u>I DMGGASVQIAFEIA-NE</u>
Y71KD	165	<u>PEVSDHPTFGFM</u>	<u>D MGGASTQIAF--APHDS</u>

FIG. 3D

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GTGGGGTCGT ATCCCGCGGG TGGAGGCCGG GGTGGCGCGG GCCGGGCGG GGGAGCCCA 60
AAGACCGGCT GCCGCCTGCT CCCCCGAAA GGCACCTCGT CTCCGTGGGT GTGGCGGAGC 120
GCGCGGTGCA TGGAAATGGC TATGTGAATG AAAAAAGTA TCCGTTATGA AACTTCCAGA 180
AAAACGAGCT ACATTTTCA GCAGCCGCAG CACGGTCCTT GGCAACAAG G ATG AGA 237
Met Arg
1
AAA ATA TCC AAC CAC GGG AGC CTG CCG GTG GCG AAG GTG GCA TAC CCC 285
Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro
5 10 15
CTG GGG CTG TGT GTG GGC GTG TTC ATC TAT GTT GCC TAC ATC AAG TGG 333
Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp
20 25 30
CAC CGG GCC ACC GCC ACC CAG GCC TTC TTC AGC ATC ACC AGG GCA GCC 381
His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala
35 40 45 50

FIG. 4A



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CCG GGG GCC CGG TGG GGT CAG CAG GCC CAC AGC CCC CTG GGG ACA GCT	429
Pro Gly Ala Arg Trp Gly Gln Ala His Ser Pro Leu Gly Thr Ala	65
	60
GCA GAC GGG CAC GAG GTC TTC TAC GGG ATC ATG TTT GAT GCA GGA AGC	477
Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser	80
	75
ACT GGC ACC CGA GTA CAC GTC TTC CAG TTC ACC CGG CCC CCC AGA GAA	525
Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu	95
	90
ACT CCC ACG TTA ACC CAC GAA ACC TTC AAA GCA GTG AAG CCA GGT CTT	573
Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu	110
	105
TCT GCC TAT GCT GAT GAT GTT GAA AAG AGC GCT CAG GGA ATC CGG GAA	621
Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu	125
	120
	130

FIG. 4B



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CTA CTG GAT GTT GCT AAA CAG GAC ATT CCG TTC GAC TTC TGG AAG GCC Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala 135 140 145	669
ACC CCT CTG GTC CTC AAG GCC ACA GCT GGC TTA CGC CTG TTA CCT GGA Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Gly 150 155 160	717
GAA AAG GCC CAG AAG TTA CTG CAG AAG GTG AAA GAA GTA TTT AAA GCA Glu Lys Ala Gln Lys Leu Lys Leu Gln Lys Val Lys Glu Val Phe Lys Ala 165 170 175	765
TCG CCT TTC CTT GTA GGG GAT GAC TGT GTT TCC ATC ATG AAC GGA ACA Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn Gly Thr 180 185 190	813
GAT GAA GGC GTT TCG GCG TGG ATC ACC ATC AAC TTC CTG ACA GGC AGC Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser 195 200 205 210	861
TTG AAA ACT CCA GGA GGG AGC AGC GTG GGC ATG CTG GAC TTG GGC GGA Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly 215 220 225	909



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GGA TCC ACT CAG ATC GCC TTC CTG CCA CGC GTG GAG GGC ACC CTG CAG 957
Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln
230 235 240

GCC TCC CCA CCC GGC TAC CTG ACG GCA CTG CGG ATG TTT AAC AGG ACC 1005
Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr
245 250 255

TAC AAG CTC TAT TCC TAC AGC TAC CTC GGG CTC GGG CTG ATG TCG GCA 1053
Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Met Ser Ala
260 265 270

CGC CTG GCG ATC CTG GGC GGC GTG GAG GGC CAG CCT GCT AAG GAT GGA 1101
Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys Asp Gly
275 280 285 290

AAG GAG TTG GTC AGC CCT TGC TTG TCT CCC AGT TTC AAA GGA GAG TGG 1149
Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp
295 300 305

GAA CAC GCA GAA GTC ACG TAC AGG GTT TCA GGG CAG AAA GCA GCG GCA 1197
Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala
310 315 320

FIG. 4D



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AGC CTG CAC GAG CTG TGT GCT GCC AGA GTG TCA GAG GTC CTT CAA AAC	1245
Ser. Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn	
325 330 335	
AGA GTG CAC AGG ACG GAG GAA GTG AAG CAT GTG GAC TTC TAT GCT TTC	1293
Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe	
340 345 350	
TCC TAC TAT TAC GAC CTT GCA GCT GGT GTG GGC CTC ATA GAT GCG GAG	1341
Ser Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu	
355 360 365 370	
AAG GGA GGC AGC CTG GTG GTG GGG GAC TTC GAG ATC GCA GCC AAG TAC	1389
Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala Lys Tyr	
375 380 385	
GTG TGT CGG ACC CTG GAG ACA CAG CCG CAG AGC AGC CCC TTC TCA TGC	1437
Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys	
390 395 400	
ATG GAC CTC ACC TAC GTC AGC CTG CTA CTC CAG GAG TTC GGC TTT CCC	1485
Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly Phe Pro	
405 410 415	



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AGG AGC AAA GTG CTG AAG CTC ACT CGG AAA ATT GAC AAT GTT GAG ACC 1533
Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr
420 425 430

AGC TGG GCT CTG GGG GCC ATT TTT CAT TAC ATC GAC TCC CTG AAC AGA 1581
Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg
435 440 445 450

CAG AAG AGT CCA GCC TCA TAGTGGCCGA GCCATCCCTG TCCCCGTCAG 1629
Gln Lys Ser Pro Ala Ser
455

CAGTGTCTGT GTGTCTGCAAT AAACCCCTCCT GTCCCTGGACG TGA CTTTCATC CTGAGGAGCC 1689

ACAGCACAGG CCGTGTGGC ACTTTCGCA CACTGGCTCT GGGACTTGCA GAAGGCCCTGG 1749

TGCTGCCCTG GCATCAGCCT CTTCCAGTCA CATCTGGCCA GAGGGCTGTC TGGACCTGGG 1809

CCCTGTCTAA TGCCACCTGT CTGCCTGGGC TCCAAGTGGG CAGGACCAGG ACAGAACCAC 1869

AGGCACACAC TGAGGGGGCA GTGTGGCTCC CTGCCTGTCC CATCCCCATG CCCCCTCCGC 1929

FIG. 4F



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GGGGCTGTGG CTGCTGCTGT GCATGTCCCT GCGATGGGAG TCTTGCTCC CAGCCTGTCA 1989
GTTTCCTCCC CAGGGCAGAG CTCCCCCTCC TGCAAGAGTC TGGAGGCGG TGCAGGCTGT 2049
CCTGGCTGCT CTGGGGAAGC CGAGGGACAG CCATAACACC CCCGGGACAG TAGGTCTGGG 2109
CGGCACCACT GGGAACTCTG GACTTGAGTG TGTTGCTCT TCCTTGGGTA TGAATGTGTG 2169
AGTTCACCCA GAGGCCTGCT CTCCTCACAC ATTGTGTGGT TTGGGGTTAA TGATGGAGGG 2229
AGACACCTCT TCATAGACGG CAGGTGCCCCA CCTTTCAGG AGTCTCCCAG CATGGGCGGA 2289
TGCCGGGCAT GAGCTGCTGT AACTATTG TGGCTGTGCT GCTTGAGTGA CGTCTCTGTC 2349
GTGTGGGTGC CAAGTGCTTG TGTAAGAACT GTGTTCTGAG CCCCCTTTC TGGACACCAA 2409
CTGTGTCCCTG TGAATGTATC GCTACTGTGA GCTGTTCCCG CCTAGCCAGG GCCATGTCTT 2469
AGGTGCAGCT GTGCCACGGG TCAGCTGAGC CACAGTCCCA GAACCAAGCT CTCGGTGTCT 2529

FIG. 4G



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CGGGCCACCA TCGGGCCACC TCGGGCTGAC CCCACCTCCT CCATGGACAG TGTGAGCCCC 2589
GGGCGGTGCA TCCTGCTCAG TGTGGCGTCA GTGTCGGGGC TGAGCCCCCTT GAGCTGCTTC 2649
AGTGAATGTA CAGTGCCCGG CACGAGCTGA ACCTCATGTG TTCCACTCCC AATAAAAGGT 2709
TGACAGGGGC TTCTCCTTCA AAAAAAAAAA AAAAAAAAAA AAA 2762

FIG. 4H



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FIG. 5A

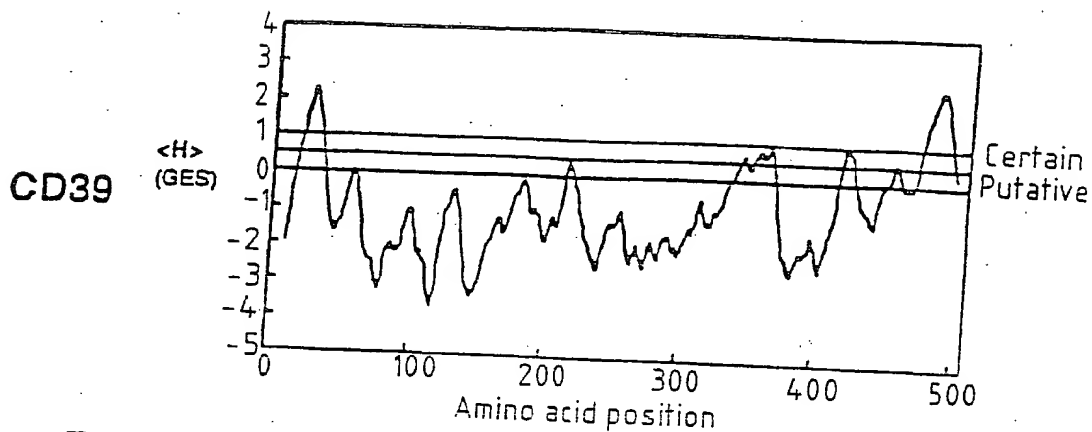


FIG. 5B

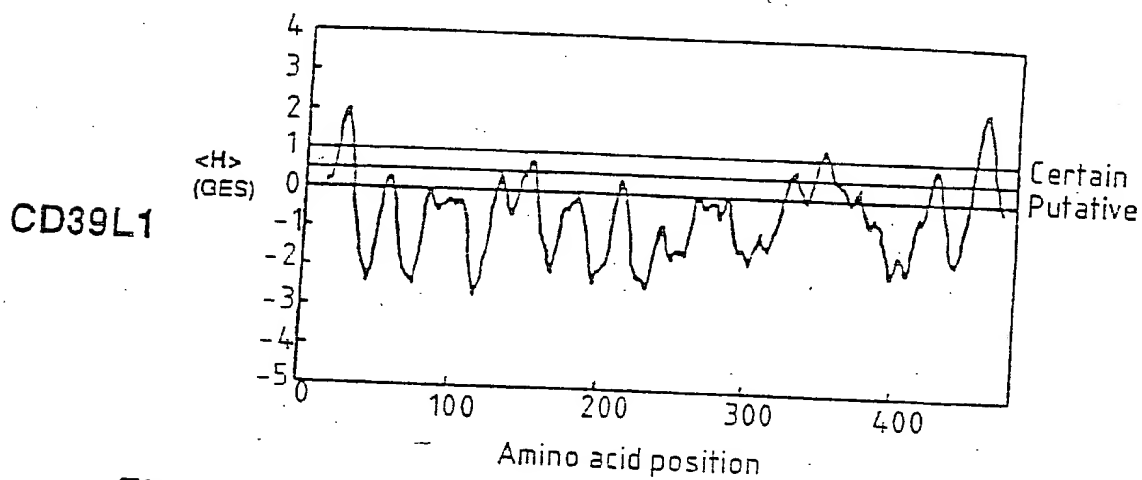
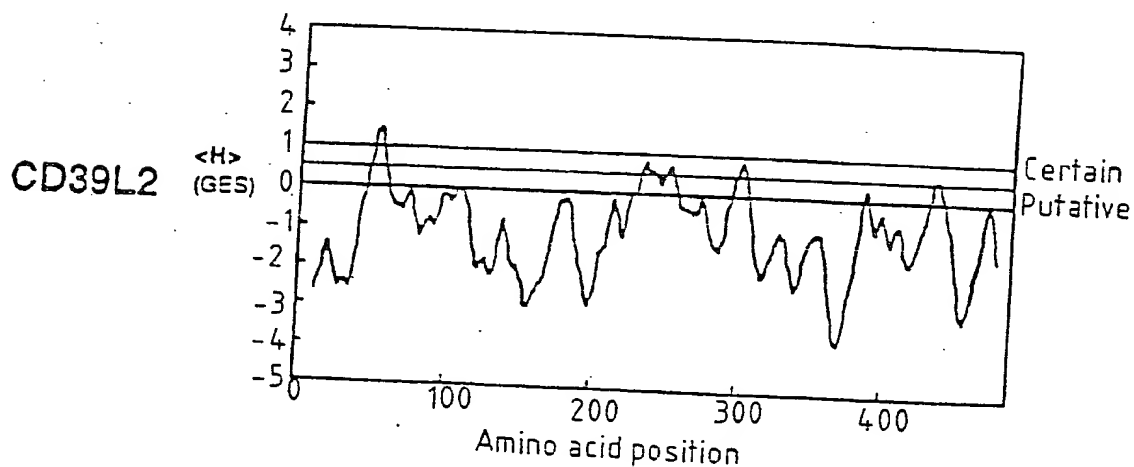
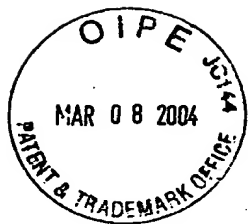


FIG. 5C





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FIG. 5D

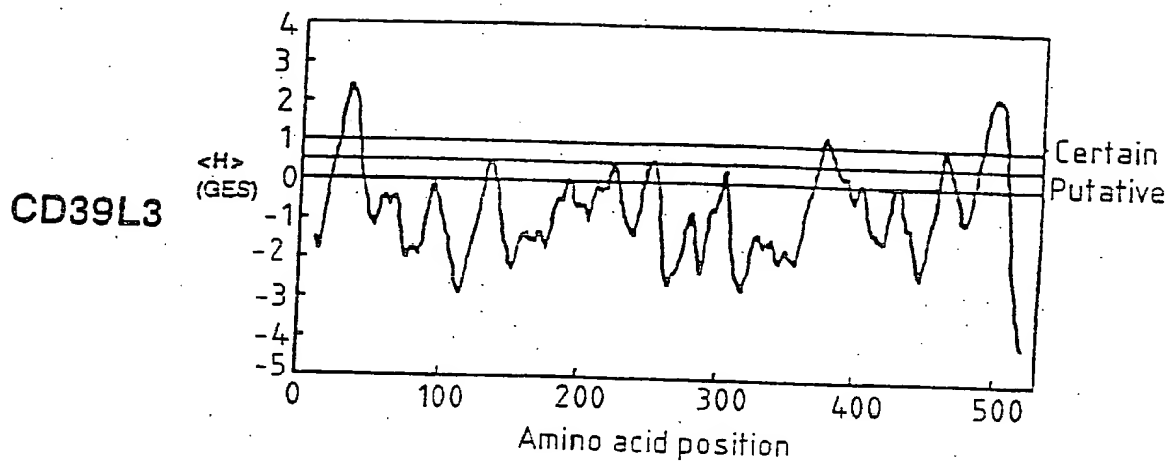
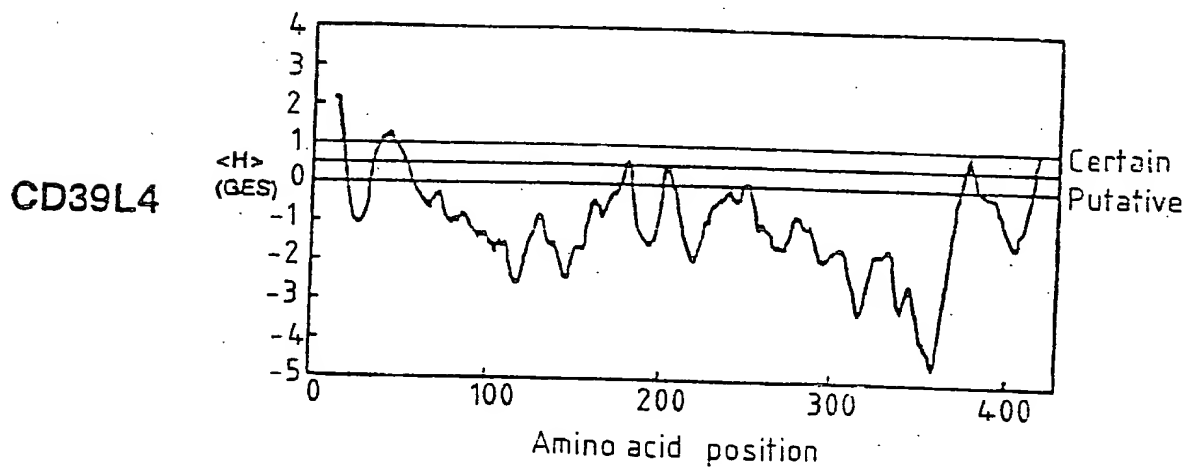


FIG. 5E





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ACCCACGGGT CTGGCCGGGG GCCGCCTCTG CGGCAGCGGT AGTCGCCTTC TCCGAATCGG 60

CTCCGCACAG CTAGGAGAAA AG ATG TTC ACT GTG CTG ACC CGC CAA CCA TGT 112
Met Phe Thr Val Leu Thr Arg Gln Pro Cys 10
1 5

GAG CAA GCA GGC CTC AAG GCC CTC TAC CGA ACT CCA ACC ATC ATT GCC 160
Glu Gln Ala Gly Leu Lys Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala 25
15 20

TTG GTG GTC TTG CTT GTG AGT ATT GTG GTA CTT GTG AGT ATC ACT GTC 208
Leu Val Val Leu Leu Val Ser Ile Val Val Leu Val Ser Ile Thr Val 40
30 35

ATC CAG ATC CAC AAG CAA GAG GTC CTC CCT CCA GGA CTG AAG TAT GGT 256
Ile Gln Ile His Lys Gln Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly 50
45 55

ATT GTG CTG GAT GCC GGG TCT TCA AGA ACC ACA GTC TAC GTG TAT CAA 304
Ile Val Leu Asp Ala Gly Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln 60
65 70

FIG. 6A



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TGG CCA GCA GAA AAA GAG AAT AAT ACC GGA GTG GTC AGT CAA ACC TTC	352
Trp Pro Ala Glu Lys Glu Asn Thr Gly Val Ser Gln Thr Phe	90
75	85
AAA TGT AGT GTG AAA GGC TCT GGA ATC TCC AGC TAT GGA AAT AAC CCC	400
Lys Cys Ser Val Lys Gly Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro	105
95	100
caa gat gtc ccc aga gcc ttt gag gag tgt atg caa aaa gtc aag ggg	448
Gln Asp Val Pro Arg Ala Phe Glu Glu Cys Met Gln Lys Val Lys Gly	120
110	115
CAG GTT CCA TCC CAC CTC CAC GGA TCC ACC CCC ATT CAC CTG GGA GCC	496
Gln Val Pro Ser His Leu His Gly Ser Thr Pro Ile His Leu Gly Ala	135
125	130
ACG GCT GGG ATG CGC TTG CTG AGG TTG CAA AAT GAA ACA GCA GCT AAT	544
Thr Ala Gly Met Arg Leu Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn	150
140	145
GAA GTC CTT GAA AGC ATC CAA AGC TAC TTC AAG TCC CAG CCC TTT GAC	592
Glu Val Leu Glu Ser Ile Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp	170
155	160

FIG. 6B

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TTT AGG GGT GCT CAA ATC ATT TCT GGG CAA GAA GAA GGG GTA TAT GGA	640
Phe Arg Gly Ala Gln Ile Ile Ser Gly Gln Glu Glu Gly Val Tyr Gly	185
	175
	180
TGG ATT ACA GCC AAC TAT TTA ATG GGA AAT TTC CTG GAG AAG AAC CTG	688
Trp Ile Thr Ala Asn Tyr Leu Met Gly Asn Phe Leu Glu Lys Asn Leu	200
	190
	195
TGG CAC ATG TGG GTG CAC CCG CAT GGA GTG GAA ACC ACG GGT GCC CTG	736
Trp His Met Trp Val His Pro His Gly Val Glu Thr Thr Gly Ala Leu	210
	205
	215
GAC TTA GGT GGT GCC TCC ACC CAA ATA TCC GTG GCA GGA GAG AAG	784
Asp Leu Gly Gly Ala Ser Thr Gln Ile Ser Phe Val Ala Gly Glu Lys	225
	220
	230
ATG GAT CTG AAC ACC AGC GAC ATC ATG CAG GTG TCC CTG TAT GGC TAC	832
Met Asp Leu Asn Thr Ser Asp Ile Met Gln Val Ser Leu Tyr Gly Tyr	240
	235
	245
GTA TAC ACG CTC TAC ACA CAC AGC TTC CAG TGC TAT GGC CGG AAT GAG	880
Val Tyr Thr Leu Tyr Thr His Ser Phe Gln Cys Tyr Gly Arg Asn Glu	255
	250
	260
	265

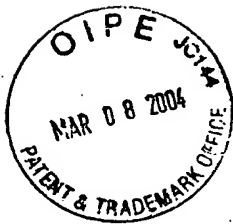
FIG. 6C



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GCT GAG AAG AAG TTT CTG GCA ATG CTC CTG CAG AAT TCT CCT ACC AAA Ala Glu Lys Lys Phe Leu Ala Met Leu Leu Gln Asn Ser Pro Thr Lys	270 275 280	928
AAC CAT CTC ACC AAT CCC TGT TAC CCT CGG GAT TAT AGC ATC AGC TTC Asn His Leu Thr Asn Pro Cys Tyr Pro Arg Asp Tyr Ser Ile Ser Phe	285 290 295	976
ACC ATG GGC CAT GTA TTT GAT AGC CTG TGC ACT GTG GAC CAG AGG CCA Thr Met Gly His Val Phe Asp Ser Leu Cys Thr Val Asp Gln Arg Pro	300 305 310	1024
GAA AGT TAT AAC CCC AAT GAT GTC ATC ACT TTT GAA GGA ACT GGG GAC Glu Ser Tyr Asn Pro Asn Asp Val Ile Thr Phe Glu Gly Thr Gly Asp	315 320 325 330	1072
CCA TCT CTG TGT AAG GAG AAG GTG GCT TCC ATA TTT GAC TTC AAA GCT Pro Ser Leu Cys Lys Glu Lys Val Ala Ser Ile Phe Asp Phe Lys Ala	335 340 345	1120
TGC CAT GAT CAA GAA ACC TGT TCT TTT GAT GGG GTT TAT CAG CCA AAG Cys His Asp Gln Glu Thr Cys Ser Phe Asp Gly Val Tyr Gln Pro Lys	350 355 360	1168

FIG. 6D



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ATT AAA GGG CCA TTT GTG GCT TTT GCA GGA TTC TAC TAC ACA GCC AGT 1216
Ile Lys Gly Pro Phe Val Ala Phe Ala Gly Phe Tyr Tyr Thr Ala Ser 375
365

GCT TTA AAT CTT TCA GGT AGC TTT TCC CTG GAC ACC TTC AAC TCC AGC 1264
Ala Leu Asn Leu Ser Gly Ser Phe Ser Leu Asp Thr Phe Asn Ser Ser 390
380 385

ACC TGG AAT TTC TGC TCA CAG AAT TGG AGT CAG CTC CCA CTG CTG CTC 1312
Thr Trp Asn Phe Cys Ser Gln Asn Trp Ser Gln Leu Pro Leu Leu Leu 400 405
395 410

CCC AAA TTT GAT GAG GTA TAT GCC CGC TCT TAC TGC TTC TCA GCC AAC 1360
Pro Lys Phe Asp Glu Val Tyr Ala Arg Ser Tyr Cys Phe Ser Ala Asn 420 425
415

TAC ATC TAC CAC TTG TTT GTG AAC GGT TAC AAA TTC ACA GAG GAG ACT 1408
Tyr Ile Tyr His Leu Phe Val Asn Gly Tyr Lys Phe Thr Glu Glu Thr 430 435 440

TGG CCC CAA ATA CAC TTT GAA AAA GAA GTG GGG AAT AGC AGC ATA GCC 1456
Trp Pro Gln Ile His Phe Glu Lys Glu Val Gly Asn Ser Ser Ile Ala 445 450 455

FIG. 6E



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TGG TCT CTT GGC TAC ATG CTC AGC CTG ACC AAC CAG ATC CCA GCT GAA 1504
Trp Ser Leu Gly Tyr Met Leu Ser Leu Thr Asn Gln Ile Pro Ala Glu
460 465 470

AGC CCT CTG ATC CGT CTG CCC ATA GAA CCA CCT GTC TTT GTG GGC ACC 1552
Ser Pro Leu Ile Arg Leu Pro Ile Glu Pro Pro Val Phe Val Gly Thr
475 480 485 490

CTC GCT TTC ACA GTG GCA GCC TTG CTG TGT CTG GCA TTT CTT GCA 1600
Leu Ala Phe Phe Thr Val Ala Ala Leu Leu Cys Leu Ala Phe Leu Ala
495 500 505

TAC CTG TGT TCA GCA ACC AGA AGA AAG AGG CAC TCC GAG CAT GCC TTT 1648
Tyr Leu Cys Ser Ala Thr Arg Arg Lys Arg His Ser Glu His Ala Phe
510 515 520

GAC CAT GCA GTG GAT TCT GAC TGAGCCTTCA AAGCAGCTCC TGGAGTCCAA 1699
Asp His Ala Val Asp Ser Asp
525

TGGCTGCTTA GAGTCAGCCT GGGTGGCACC AGGCAATGCA GGTAAGTGG CTGCCTTCAG 1759



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GAAATACAAC TAACTAAAAT CAAACACCTA GGTACAGTGC CTCTCAAATA CTGATTCTG 1819
CCACAGCACC TCTTGAGGCA TCCCTTGGCT ATTCTGTGCA TATTGTTCTT CAGAGACCTC 1879
ACTACCCACA TGCTGATCTA TTGGGGAACA GAGAAGAGAC AGGCCACTAA GGTCAGGCTC 1939
TTTATATTAA GTTCCCCAGA GGAAGAGTAA GTTGAGAAGG TATCAGTTTA ATGTTGAAGA 1999
ATTGACCTCA GGGCTCAGTT TCCATTCCC TCCCTCAGTA TTCTTCCTGG CAAGATACCC 2059
ATTAAGCAAT TCGCCAAATCA GAATCTCAT TTTATAGTTTT TCCCATTGGT CTTTAACTAA 2119
GACTTTCTTG TAGCAATCTC GTAAGCAGTG AACCCCTCA GATCAGTAGA ATATAGTATC 2179
TGGGGGAGAA GACTTACTTC CTTCAGGGCA GCAGCCACAG CCAGGCTTCT GTCATACAGG 2239
TAGATCCCGA AGCACAGAGA CATAAAAAG GTCTCCCAGA AAATATAGA CCATTCTCCA 2299
AGTGAATTC CCACTTAGG CTCGTGTCAC TAGATTGCAA CCTGTGTGTT TGCATCATC 2359
CTCATCTCAC CATTGTATTG CTATGCCCTC CCATAAAAC ACATTGATCC CTAGCAAGAT 2419



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TATTGCATTG CAGATTTTAC TGCCTTTGCT AGGCTTTTGC TTAGCAAAGG GCTGACTTTC 2479
CATTGTTATC ATGGTGATA TATTTTGTG ACCATTCCCA CAAGTATACT TGATGTTGTC 2539
ATAGAACGAA CATCCTACTC TATGATTTAC TAACCAATTA CTTTCCCGA TCATAGACCT 2599
CTCTGCATAG TAGTCATAGG TCTTGACTTT GGGGAAAGAA AAGGAAGCTG CAGGAATATT 2659
TATCTCCAAA GTCGAATGAG AAAGAACTCC AGCAAATCCA ATGGCTACAA ACTAAAAATC 2719
AGCATTATTT CATATTGCTG TTTCTTAGCT GAATATGGAA TAAAGAACTA TTATTTTATT 2779
TTGAAAAAAA AAAAAAAA 2797

FIG. 6H



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FIG. 7A

GGCGCGCGGT TTTCCTTGTT CCTGGTCAAC AAAGAAATGT GGAGTGTCTT GGCTGAATCC 60
TCATACAGAC AAGATCATTA TGGTGCTGTT AGGTAGGACT TGTATCCAGA TGTAAGGTG 120
AAAAAGTGAT ATAATAAAGG AACCAAGGAG AAAATTCAGA AGGAAAGAAA AAATTGCCCTC 180
TGCAGGTGTG CGAGCAGGAT TGCTTCTGCA ACAAAGCCT CCACCCAGCC ACATCTTGGG 240
AAAAAG ATG GCC ACT TCT TGG GGC ACA GTC TTT TTC ATG CTG GTG GTA 288
Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val 10
1 5
TCC TGT GTT TGC AGC GCT GTC TCC CAC AGG AAC CAG CAG ACT TGG TTT 336
Ser Cys Val Cys Ser Ala Val Ser His Arg Asn Gln Thr Trp Phe 25 30
15 20
GAG GGT ATC TTC CTG TCT TCC ATG TGC CCC ATC AAT GTC AGC GCC AGC 384
Glu Gly Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser 35 40 45
ACC TTG TAT GGA ATT ATG TTT GAT GCA GGG AGC ACT GGA ACT CGA ATT 432
Thr Leu Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile 50 55 60



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CAT GTT TAC ACC TTT GTG CAG AAA ATG CCA GGA CAG CTT CCA ATT CTA His Val Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu 65 70 75 480
GAA GGG GAA GTT TTT GAT TCT GTG AAG CCA GGA CTT TCT GCT TTT GTA Glu Gly Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val 80 85 90 528
GAT CAA CCT AAG CAG GGT GCT GAG ACC GTT CAA GGG CTC TTA GAG GTG Asp Gln Pro Lys Gln Ala Glu Thr Val Gln Gly Leu Leu Glu Val 95 100 105 576
GCC AAA GAC TCA ATC CCC CGA AGT CAC TGG AAA AAG ACC CCA GTG GTC Ala Lys Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val 110 115 120 125 624
CTA AAG GCA ACA GCA GGA CTA CGC TTA CTG CCA GAA CAC AAA GCC AAG Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys 130 135 140 672
GCT CTG CTC TTT GAG GTA AAG GAG ATC TTC AGG AAG TCA CCT TTC CTG Ala Leu Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu 145 150 155 720



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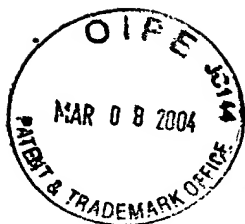
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FIG. 7C

GTA CCA AAG GGC AGT GTT AGC ATC ATG GAT GGA TCC GAC GAA GGC ATA	768
Val Pro Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile	
160 165 170	
TTA GCT TGG GTT ACT GTG AAT TTT CTG ACA GGT CAG CTG CAT GGC CAC	816
Leu Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His	
175 180 185 190	
AGA CAG GAG ACT GTG GGG ACC TTG GAC CTA GGG GGA GCC TCC ACC CAA	864
Arg Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln	
195 200 205	
ATC ACG TTC CTG CCC CAG TTT GAG AAA ACT CTG GAA CAA ACT CCT AGG	912
Ile Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg	
210 215 220	
GGC TAC CTC ACT FCC TTT GAG ATG TTT AAC AGC ACT TAT AAG CTC TAT	960
Gly Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr	
225 230 235	
ACA CAT AGT TAC TTG GGA TTT GGA TTG AAA GCT GCA AGA CTA GCA ACC	1008
Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr	
240 245 250	



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CTG GGA GCC CTG GAG ACA GAA GGG ACT GAT GGG CAC ACT TTC CGG AGT	1056
Leu Gly Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser	255 260 265 270
GCC TGT TTA CCG AGA TGG TTG GAA GCA GAG TGG ATC TTT GGG GGT GTG	1104
Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val	275 280 285
AAA TAC CAG TAT GGT GGC AAC CAA GAA GGG GAG GTG GGC TTT GAG CCC	1152
Lys Tyr Gln Tyr Glu Gly Glu Asn Gln Glu Gly Glu Val Gly Phe Glu Pro	290 295 300
TGC TAT GCC GAA GTG CTG AGG GTG GTA CGA GGA AAA CTT CAC CAG CCA	1200
Cys Tyr Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro	305 310 315
GAG GAG GTC CAG AGA GGT TCC TTC TAT GCT TTC TCT TAC TAT TAT GAC	1248
Glu Glu Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp	320 325 330
CGA GCT GTT GAC ACA GAC ATG ATT GAT TAT GAA AAG GGG GGT ATT TTA	1296
Arg Ala Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu	335 340 345 350

FIG. 7D



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AAA GTT GAA GAT TTT GAA AGA AAA GCC AGG GAA GTG TGT GAT AAC TTG 1344
Lys Val Glu Asp Phe 355
360
365
GAA AAC TTC ACC TCA GGC AGT CCT TTC CTG TGC ATG GAT CTC AGC TAC 1392
Glu Asn Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr
370 375 380
ATC ACA GCC CTG TTA AAG GAT GGC TTT GGC TTT GCA GAC AGC ACA GTC 1440
Ile Thr Ala Leu Leu Lys Asp Gly Phe Phe Ala Asp Ser Thr Val
385 390 395
TTA CAG CTC ACA AAG AAA GTG AAC ATA GAG ACG GGC TGG GCC TTG 1488
Leu Gln Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu
400 405 410
GGG GCC ACC TTT CAC CTG TTG CAG TCT CTG GGC ATC TCC CAT 1530
Gly Ala Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His
415 420 425
TGAGGCCACG TACTTCCTTG GAGACCTGCA TTGCGCAACA CCTTTTAAAG GGGAGGAGAG 1590



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AGCACTTAGT TTCTGAACTA GTCTGGGACA TCCTGGACTT GAGCCTAGAG ATTTAGGTTT 1650
AATTAAATTT ACACATCTAA TGTGAACTGC TGCCTAACCA CTCAGAGTA CACAGCTGGC 1710
ACCAGAGCAT CACAGAGAGC CCTGTGAGCC AAAAAGTATA GTTTTGGAAC TTAACCTTGG 1770
AGTGAGAGCC CAGGGACAGG TCCCTGGAAA CCAAAGAAAA ATCGCATTTC AACCCTTTGA 1830
GTGCCTCATT CCACTGAATA TTAAATTTT CCTCTTAAAT GGTAAACTGA CTTATTGCAA 1890
TCCCAAGACC CATCAATATC AGTATTTTTT TCCTCCCCTAT ACAGTGCCCTT GCCCACCCCTT 1950
ATCTGCACCC ACCTCCCCTG AAAAAGAGAG AAAAAAAAAA AAAAAAAA 1998

FIG. 7F



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CD39L2	1	MKKGIRYETSRKTSYIFQQPQHGPWQTRMRKISNHGSLRVAKVAYPLGLCVGVFIYVAYI	
CD39L4	1	-----	
CD39L1	1	-----MATSWG	
CD39L3	1	-----	
CD39	1	-----MFTVLTRQPCQAGL	
		-----MEDTKE	
CD39L2	61	KWHRATATQAFFSITRAAPGARWGQAH-SPLGTAADGHEVFYGYIMF	ACR I
CD39L4	7	TVFFMLVVCVCSAVSHRNQQTWFEIGIFLSSMCPINVSASTLYGYIMF	DAGSTGTRVHVFPQ
CD39L1	1	---MAGKVRSLPPLLLAAAGLAGLLLCVPTRDVREP?ALKYGIIVL	DAGSTGTRI HVYT
CD39L3	16	KALYRTPTIIALVVLVLSIVVLVSTVVIQIHKQEVLP-PGGLKYGIIVL	DAGSSHTSMFIYK
CD39	7	SNVKTFCSKNILAILGFSIIAIVIALLAUGLTONKALPENVKYGIIVL	DAGSSRTTVVYVQ
			DAGSSHTSLYIYK
CD39L2	120	FT-RPPRETPTLTHTFKAVK-PGLSAYADDVEKSAQGIRELDDVAKQDIPFDFWKATPL	ACR II
CD39L4	67	FVQKMPGQLPILEGEVFDVSK-PGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHWKKTPV	
CD39L1	58	WPADKENDTGIVGQHSSCDVPGGGISSYADNP SGASQSLVGCLEQALQDVPKERHAGTPL	
CD39L3	75	WPAEKENNTGVVSQTFKCSVKSGSISYGNPNQDVPRAFEECMQKVKGQVPSHLHGSTPI	
CD39	67	WPAEKENDTGVVHQVEECRAVKGPGISKFVKVNEIGIYLTDCMERAREVIPRSQHQETPV	

FIG. 8A



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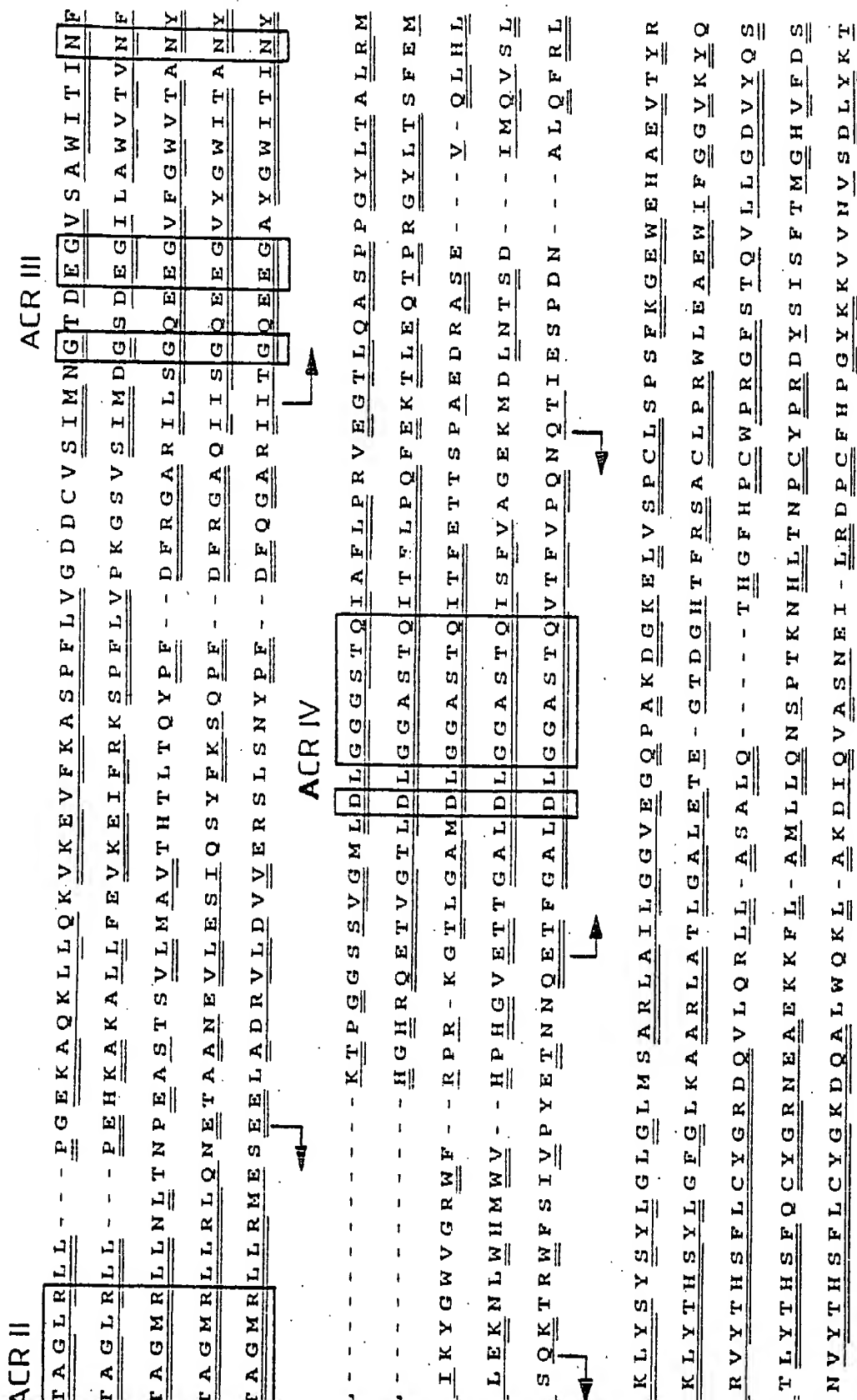
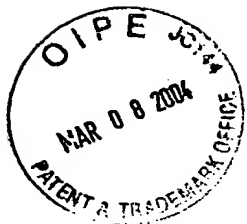


FIG. 8B



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AND NUCLEIC ACIDS

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CD39L2 343 VSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFFYAFSYYDLAAGVGLIDAEEKGGS

CD39L4 290 YGGNQEGEVGFEPCEYAEVLRVVRGKHLHQPEEVQSGSFYAFSYYDRAVDTDMDIYEKGGI

CD39L1 283 PCTMAQRPQNFNSARVSLSGSSDPHLCRDLVSGLFSFSSC-PFSRCSFNGVFQPPVAGN

CD39L3 307 LCTVDQRPESYNPNNDVITFEGTGDPSSLCKEKVASIFDFKACHDQETCSFDGVYQPKIKGP

CD39 300 PCT--KRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYC-PYSQCAFNGIFLPPPLQGD

CD39L2 403 LVVGDFEIAAKYVCRTLETQPQSSPFS CMDLTYVSLLLQE-FGFPRSKVLKLT RKIDNVE

CD39L4 350 LKVEDFERKAREVCDNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQLTKKVNNE

CD39L1 342 FV-----AFSAFFYTVDFLRTSMGLPVATLQQLEAAAVNVCNQ TWAQ-----

CD39L3 367 FV-----AFAGFYITASALNLSGSF--SLDTFNSSTWNFC SQNWSQLPLLPKFDEVY

CD39 357 FG-----AFSAFYFVMKFLNLTS--EKVSQEKVTEMKKKFCAPWEEIKTSYAGVKEKY

CD39L2 462 TSWALGAI FHYIDS LNRQKSPAS*

CD39L4 410 TGWA LGATFHL LQSLGISH

CD39L1 384 -----QLLSRGYGFDERAFGGVIFQKKAADTAVGWA LGYMLNLTNLI PADPPG

CD39L3 418 ARSYCF SANIYIYHLFVNGYKFTTEETWPQIHFFEKEVGNSSIAWS LGYMLSLTNQIPAESPL

CD39 409 LSEYCFSGTYILSLLLOGYHFTADSWEHIHF IGKIQQSDAGWTLGYMLNLTNMIPAEQP-

FIG. 8C



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CD39L2	485	
CD39L4	429	
CD39L1	432	<u>LR</u> <u>KG</u> <u>TD</u> <u>PS</u> <u>SW</u> <u>VV</u> <u>LL</u> <u>LL</u> <u>FA</u> <u>SALL</u> <u>AA</u> <u>LV</u> <u>LL</u> <u>LR</u> <u>QV</u> <u>HS</u> <u>AK</u> <u>LP</u> <u>ST</u> <u>I</u> *
CD39L3	478	<u>IR</u> <u>LP</u> <u>IE</u> <u>PP</u> <u>VF</u> <u>VG</u> <u>TL</u> <u>AF</u> <u>FT</u> <u>VAA</u> <u>LL</u> <u>CL</u> <u>AF</u> <u>LA</u> <u>YL</u> <u>CS</u> <u>AT</u> <u>RR</u> <u>KRR</u> <u>H</u> <u>SE</u> <u>HA</u> <u>FD</u> <u>HA</u> <u>VD</u> <u>SD</u> *
CD39	468	<u>LS</u> <u>TP</u> <u>LS</u> <u>HS</u> <u>ST</u> <u>YV</u> <u>FL</u> <u>MV</u> <u>LS</u> <u>LV</u> <u>LF</u> <u>TV</u> <u>AI</u> <u>GI</u> <u>GL</u> <u>LI</u> <u>FI</u> <u>HK</u> <u>PS</u> <u>YF</u> <u>WK</u> <u>DM</u> <u>V</u> *

FIG. 8D



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peaGDP	1	-----M
potapyrase 1	1	-----MLNQN
CD39L2	1	MKKGIRYETSRKTSYIFQQPQHGPWQTRMRKISNHGSLRVAKVAYPLGLCVGVFIYVAYI
CD39L4	1	-----MATSWG
dNTPase	1	-----MKY EYKLLATDEKPPRRKSSGSPNASGGNRQPSGL
YGDpase	1	-----KTPE
ACRI		
peaGDP	2	ELLIKLIITFLFSPAITSSQYLGNNL-LTSRKIFLKQEEISSYAVVFFDAGSTGSRIHVV
potapyrase 6	6	SHFIFIILAIFLVLP LSLSKNVNAQI-PLRRHL LSHSE--HYAVIFDAGSTGSRVHVF
CD39L2	61	KWHRATATQAFFSITRAAPGARWGQQA-H-SPIGTAADGHEVFFYGIMFFDAGSTGTRVHVF
CD39L4	7	TVFFMLVVSVCVCSAVSHRNQQTWFEGI-FLSSMCPINVSASTLYGIMFFDAGSTGTRIHVV
dNTPase	37	KISFLCLIIISVILL L FVFGFVSENASP-YLLARLLASKFGYSKVQYAAIIDAGSTGSRVLAY
YGDpase	5	DISILPVNDEPGYLQDSKTEQNYPELADAVKSQTSQTCSEEHK YVIMIDAGSTGSRVHIY

FIG. 9A



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		ACR II																																																											
peaGDP	61	H	F	N	Q	N	L	D	L	L	H	I	G	K	G	V	E	Y	N	K	I	T	P	G	L	S	S	Y	A	N	N	P	E	Q	A	A	K	S	L	I	P	L	L	E	Q	A	E	D	V	V	P	D	D	L	Q	P	K	T	P	V	
potapyrase	63	R	F	D	E	K	L	G	L	L	P	I	G	N	N	I	E	Y	F	M	A	T	E	P	G	L	S	S	Y	A	E	D	P	K	A	A	A	N	S	L	E	P	L	L	D	G	A	E	G	V	V	P	Q	E	L	Q	S	E	T	P	L
CD39L2	119	Q	F	T	-	R	P	P	R	E	T	P	T	L	T	H	E	T	F	K	A	V	K	P	G	L	S	A	Y	A	D	D	V	E	K	S	A	Q	G	I	R	E	L	L	D	V	A	K	Q	D	I	P	F	D	F	W	K	A	T	P	L
CD39L4	66	T	F	V	Q	K	M	P	G	Q	L	P	I	L	E	G	E	V	F	D	S	V	K	P	G	L	S	A	F	V	D	Q	P	K	Q	G	A	E	T	V	Q	G	L	L	E	V	A	K	D	S	I	P	R	S	H	W	K	T	P	V	
dNTPase	96	K	F	N	R	S	F	I	D	N	K	L	V	L	Y	E	E	L	F	F	K	E	R	K	P	G	L	S	S	F	A	D	N	P	A	E	G	A	H	S	I	K	L	L	D	E	A	R	A	F	I	P	K	E	H	W	S	T	P	L	
YGDpase	65	K	F	D	-	-	V	C	T	S	P	P	T	L	L	D	E	K	F	D	M	L	E	P	G	L	S	S	F	D	T	D	S	V	G	A	A	N	S	L	D	P	L	L	K	V	A	M	N	Y	V	P	I	K	A	R	S	C	T	P	V
		ACR II																																																											
peaGDP	121	R	L	G	A	T	A	G	L	R	L	L	N	G	D	A	S	E	K	I	L	Q	S	V	R	D	M	L	S	N	R	S	T	F	-	N	V	Q	P	D	A	V	S	I	I	D	G	T	Q	E	G	S	Y	L	W	V	T	V	N	Y	A
potapyrase	123	E	L	G	A	T	A	G	L	R	M	L	K	G	D	A	A	E	K	I	L	Q	A	V	R	N	L	V	K	N	Q	S	T	F	-	H	S	K	D	Q	W	V	T	I	L	D	G	T	Q	E	G	S	Y	M	W	A	A	I	N	Y	L
CD39L2	178	V	L	K	A	T	A	G	L	R	L	L	P	G	E	K	A	Q	X	L	L	Q	K	V	K	E	V	F	K	-	A	S	P	F	-	L	V	G	D	D	C	V	S	I	M	N	G	T	D	E	G	V	S	A	W	I	T	I	N	F	L
CD39L4	126	V	L	K	A	T	A	G	L	R	L	L	P	E	H	K	A	K	A	L	L	F	E	V	K	E	I	F	R	-	K	S	P	F	-	L	V	P	K	G	S	V	S	I	M	D	G	S	D	E	G	I	L	A	W	V	T	V	N	F	L
dNTPase	156	V	L	K	A	T	A	G	L	R	L	L	P	A	S	K	A	E	N	I	L	N	A	V	R	D	L	F	A	-	K	S	E	F	-	S	V	D	M	D	A	V	E	I	M	D	G	T	D	E	G	I	F	S	W	F	T	V	N	F	L
YGDpase	123	A	V	K	A	T	A	G	L	R	L	L	G	D	A	K	S	S	K	I	L	S	A	V	R	D	H	L	E	K	D	Y	P	P	P	V	V	E	G	D	G	V	S	I	M	G	G	D	E	E	G	V	F	A	W	I	T	T	N	Y	L
		ACR III																																																											

FIG. 9B

FIG. 9C



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peaGDP	276	<u>TYSGEEFKATAYTSG-ANFNKCKNTIRKALKLNYPYQNC</u> <u>TFGGIWN</u> <u>GG--GGNGQKN</u>
potapyrase	277	<u>SYGGVDYKVKAPKKG-SSWKRCLTRHALKINAKCNIEEC</u> <u>TFN</u> <u>GVWNGG--GGDGGQKN</u>
CD39L2	335	<u>EHA</u> <u>EV</u> <u>TYR</u> <u>V</u> <u>SGQKAAASLHELCAAR--VSEV</u> <u>-----LQNRV</u> <u>-----HRT</u> <u>-----EEVKHVD</u>
CD39L4	282	<u>IFGGVKYQYGGNQEGEVGFPCYAE--VLRV</u> <u>-----VRGKL</u> <u>-----HQP</u> <u>-----EEVQRGS</u>
dNTPase	308	<u>TYGNVQYKVS</u> <u>SGKENGKSSAEQPIVDFDACL</u> <u>EL--VKSKVMP</u> <u>LVKPKP--FTLKQHA</u>
YGD Pase	298	<u>LESKET</u> <u>Y</u> <u>T</u> <u>I</u> <u>D</u> <u>F</u> <u>I</u> <u>G</u> <u>P</u> <u>D</u> <u>E</u> <u>P</u> <u>S</u> <u>G</u> <u>A</u> <u>Q</u> <u>C</u> <u>R</u> <u>F</u> <u>L</u> <u>T</u> <u>D</u> <u>E</u> <u>I</u> <u>L</u> <u>N</u> <u>K</u> <u>D</u> <u>A</u> <u>Q</u> <u>C</u> <u>S</u> <u>P</u> <u>P</u> <u>C</u> <u>S</u> <u>F</u> <u>N</u> <u>G</u> <u>V</u> <u>H</u> <u>Q</u> <u>P</u> <u>S</u> <u>L</u> <u>V</u> <u>R</u> <u>T</u> <u>P</u> <u>K</u> <u>E</u> <u>S</u> <u>N</u> <u>D</u>
peaGDP	332	<u>LFAS</u> <u>SSFF</u> <u>Y</u> <u>L</u> <u>P</u> <u>E</u> <u>D</u> <u>T</u> <u>G</u> <u>M</u> <u>V</u> <u>D</u> <u>A</u> <u>S</u> <u>T</u> <u>P</u> <u>N</u> <u>F</u> <u>I</u> <u>L</u> <u>R</u> <u>P</u> <u>V</u> <u>D</u> <u>I</u> <u>E</u> <u>T</u> <u>K</u> <u>A</u> <u>K</u> <u>E</u> <u>A</u> <u>C</u> <u>A</u> <u>L</u> <u>N</u> <u>F</u> <u>E</u> <u>D</u> <u>A</u> <u>K</u> <u>S</u> <u>T</u> <u>Y</u> <u>P</u> <u>F</u> <u>L</u> <u>D</u> <u>K</u> <u>K</u> <u>N</u> <u>V</u> <u>A</u> <u>S</u>
potapyrase	333	<u>I</u> <u>H</u> <u>A</u> <u>S</u> <u>S</u> <u>F</u> <u>F</u> <u>Y</u> <u>D</u> <u>I</u> <u>G</u> <u>A</u> <u>Q</u> <u>V</u> <u>G</u> <u>I</u> <u>V</u> <u>D</u> <u>T</u> <u>K</u> <u>F</u> <u>P</u> <u>S</u> <u>A</u> <u>L</u> <u>A</u> <u>K</u> <u>P</u> <u>I</u> <u>Q</u> <u>Y</u> <u>L</u> <u>N</u> <u>A</u> <u>A</u> <u>K</u> <u>V</u> <u>A</u> <u>C</u> <u>T</u> <u>N</u> <u>V</u> <u>A</u> <u>D</u> <u>I</u> <u>K</u> <u>S</u> <u>I</u> <u>F</u> <u>P</u> <u>K</u> <u>T</u> <u>Q</u> <u>D</u> <u>R</u> <u>N</u> <u>I</u> <u>-P</u>
CD39L2	379	<u>F</u> <u>Y</u> <u>A</u> <u>F</u> <u>S</u> <u>Y</u> <u>Y</u> <u>D</u> <u>L</u> <u>A</u> <u>A</u> <u>G</u> <u>V</u> <u>G</u> <u>L</u> <u>I</u> <u>D</u> <u>A</u> <u>E</u> <u>-K</u> <u>G</u> <u>G</u> <u>S</u> <u>L</u> <u>V</u> <u>V</u> <u>G</u> <u>D</u> <u>P</u> <u>E</u> <u>I</u> <u>A</u> <u>K</u> <u>Y</u> <u>V</u> <u>C</u> <u>R</u> <u>T</u> <u>-----LETQPQSSP</u>
CD39L4	326	<u>F</u> <u>Y</u> <u>A</u> <u>F</u> <u>S</u> <u>Y</u> <u>Y</u> <u>D</u> <u>R</u> <u>A</u> <u>V</u> <u>D</u> <u>T</u> <u>D</u> <u>M</u> <u>I</u> <u>D</u> <u>Y</u> <u>E</u> <u>-K</u> <u>G</u> <u>G</u> <u>I</u> <u>L</u> <u>K</u> <u>V</u> <u>E</u> <u>D</u> <u>F</u> <u>E</u> <u>R</u> <u>K</u> <u>A</u> <u>R</u> <u>E</u> <u>V</u> <u>C</u> <u>D</u> <u>N</u> <u>-----LENFTSGSP</u>
dNTPase	360	<u>V</u> <u>A</u> <u>A</u> <u>F</u> <u>S</u> <u>Y</u> <u>Y</u> <u>F</u> <u>E</u> <u>R</u> <u>A</u> <u>I</u> <u>E</u> <u>S</u> <u>G</u> <u>L</u> <u>V</u> <u>D</u> <u>P</u> <u>L</u> <u>-A</u> <u>G</u> <u>G</u> <u>E</u> <u>T</u> <u>T</u> <u>V</u> <u>E</u> <u>A</u> <u>Y</u> <u>R</u> <u>K</u> <u>K</u> <u>A</u> <u>Q</u> <u>E</u> <u>I</u> <u>C</u> <u>A</u> <u>I</u> <u>-----PNDE--QP</u>
YGD Pase	358	<u>I</u> <u>Y</u> <u>I</u> <u>F</u> <u>S</u> <u>Y</u> <u>Y</u> <u>D</u> <u>R</u> <u>T</u> <u>R</u> <u>P</u> <u>L</u> <u>G</u> <u>M</u> <u>P</u> <u>L</u> <u>S</u> <u>F</u> <u>T</u> <u>L</u> <u>N</u> <u>E</u> <u>L</u> <u>N</u> <u>D</u> <u>L</u> <u>A</u> <u>R</u> <u>I</u> <u>V</u> <u>C</u> <u>K</u> <u>G</u> <u>E</u> <u>E</u> <u>T</u> <u>W</u> <u>N</u> <u>S</u> <u>V</u> <u>F</u> <u>S</u> <u>G</u> <u>I</u> <u>A</u> <u>G</u> <u>S</u> <u>L</u> <u>-----DELESDS</u>

FIG. 9D



Title: METHODS AND COMPOSITIONS
RELATING TO CD-39-LIKE POLYPEPTIDES
AND NUCLEIC ACIDS

Applicants: Chadwick et al.

Docket No. 28110/36120D

46/46

peaGDP	392	<u>YV</u> <u>CMD</u> <u>L</u> <u>I</u> <u>YQ</u> <u>YV</u> <u>LL</u> <u>VD</u> <u>GG</u> <u>LD</u> <u>PL</u> <u>QK</u> <u>IT</u> <u>SG</u> <u>KE</u> <u>IE</u> <u>YQ</u> <u>DA</u> <u>I</u> <u>VE</u> <u>AA</u> <u>PL</u> <u>GN</u> <u>AVE</u> <u>A</u> <u>I</u> <u>S</u> <u>AL</u> <u>PK</u> <u>FE</u> <u>RL</u>
potapyrase	392	<u>YLC</u> <u>MD</u> <u>L</u> <u>I</u> <u>Y</u> <u>E</u> <u>Y</u> <u>TL</u> <u>LV</u> <u>D</u> <u>GG</u> <u>LN</u> <u>PH</u> <u>KE</u> <u>IT</u> <u>VI</u> <u>HD</u> <u>VQ</u> <u>YK</u> <u>NY</u> <u>LV</u> <u>GA</u> <u>AW</u> <u>PL</u> <u>GC</u> <u>AI</u> <u>D</u> <u>LV</u> <u>SS</u> <u>TT</u> <u>NK</u> <u>IR</u> <u>V</u>
CD39L2	428	<u>PSC</u> <u>MD</u> <u>L</u> <u>TY</u> <u>V</u> <u>S</u> <u>LL</u> <u>QE</u> <u>-</u> <u>FG</u> <u>FP</u> <u>RS</u> <u>KV</u> <u>LK</u> <u>L</u> <u>TR</u> <u>K</u> <u>ID</u> <u>N</u> <u>-</u> <u>-</u> <u>-</u> <u>V</u> <u>ET</u> <u>SW</u> <u>AL</u> <u>GA</u> <u>IF</u> <u>HY</u> <u>ID</u> <u>SL</u> <u>NR</u> <u>Q</u> <u>K</u> <u>SP</u>
CD39L4	375	<u>FLC</u> <u>MD</u> <u>LS</u> <u>Y</u> <u>I</u> <u>T</u> <u>AL</u> <u>LK</u> <u>D</u> <u>GG</u> <u>F</u> <u>AD</u> <u>ST</u> <u>V</u> <u>L</u> <u>Q</u> <u>L</u> <u>T</u> <u>KK</u> <u>V</u> <u>NN</u> <u>-</u> <u>-</u> <u>-</u> <u>I</u> <u>ET</u> <u>GW</u> <u>AL</u> <u>GA</u> <u>T</u> <u>F</u> <u>H</u> <u>L</u> <u>L</u> <u>Q</u> <u>S</u> <u>L</u> <u>G</u> <u>I</u> <u>S</u> <u>H</u>
dNTPase	406	<u>FMC</u> <u>FD</u> <u>L</u> <u>T</u> <u>F</u> <u>I</u> <u>ST</u> <u>LL</u> <u>R</u> <u>E</u> <u>G</u> <u>F</u> <u>GL</u> <u>ND</u> <u>GK</u> <u>K</u> <u>I</u> <u>K</u> <u>L</u> <u>Y</u> <u>KK</u> <u>ID</u> <u>G</u> <u>-</u> <u>-</u> <u>-</u> <u>H</u> <u>E</u> <u>I</u> <u>SW</u> <u>AL</u> <u>GC</u> <u>AY</u> <u>N</u> <u>V</u> <u>L</u> <u>T</u> <u>S</u> <u>D</u> <u>E</u> <u>K</u> <u>F</u> <u>S</u> <u>N</u> <u>S</u>
YGDpase	415	<u>HFC</u> <u>LD</u> <u>LS</u> <u>FQ</u> <u>V</u> <u>S</u> <u>LL</u> <u>HT</u> <u>GY</u> <u>D</u> <u>I</u> <u>P</u> <u>L</u> <u>Q</u> <u>R</u> <u>E</u> <u>L</u> <u>R</u> <u>T</u> <u>G</u> <u>K</u> <u>K</u> <u>I</u> <u>A</u> <u>N</u> <u>K</u> <u>-</u> <u>-</u> <u>-</u> <u>E</u> <u>I</u> <u>GW</u> <u>CL</u> <u>GA</u> <u>SL</u> <u>P</u> <u>L</u> <u>L</u> <u>K</u> <u>A</u> <u>D</u> <u>N</u> <u>W</u> <u>K</u> <u>C</u> <u>K</u> <u>I</u>
peaGDP	452	<u>MY</u> <u>FV</u>
potapyrase	452	<u>AS</u> <u>*</u>
CD39L2	483	<u>AS</u> <u>*</u>
CD39L4	429	
dNTPase	462	
YGDpase	471	<u>Q</u> <u>S</u> <u>A</u>

FIG. 9E